

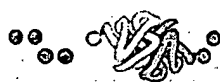


Search for

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LOCUS AAC16476 231 aa PLN 16-MAY-1998
 DEFINITION putative acyl-CoA:cholesterol acyltransferase.
 ACCESSION AAC16476
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 VERSION AAC16476.1 GI:3135276
 DBSOURCE locus ATAC003058 accession [AC003058.1](#)
 KEYWORDS .
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
 eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
 Arabidopsis.
 REFERENCE 1 (residues 1 to 231)
 AUTHORS Rounsley, S.D., Lin, X., Ketchum, K.A., Crosby, M.L., Brandon, R.C.,
 Sykes, S.M., Kaul, S., Mason, T.M., Kerlavage, A.R., Adams, M.D.,
 Somerville, C.R. and Venter, J.C.
 TITLE Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 231)
 AUTHORS Rounsley, S.D. and Lin, X.
 TITLE Direct Submission
 JOURNAL Submitted (06-NOV-1997) The Institute for Genomic Research, 9712
 Medical Center Dr, Rockville, MD 20850, USA, rounsley@tigr.org
 REFERENCE 3 (residues 1 to 231)
 AUTHORS Rounsley, S.D.
 TITLE Direct Submission
 JOURNAL Submitted (16-MAY-1998) The Institute for Genomic Research, 9712
 Medical Center Dr., Rockville, MD 20850, USA
 COMMENT Method: conceptual translation.
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 121 llyaiervlk lsvpnlyvwl cmfycffhlw lnlaellcf gdrefykdwv naksvgydwr
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Search for

as

1: AAC63997

ACAT related gene product 1 [Homo sapiens]

LOCUS AAC63997 488 aa PRI 15-OCT-1998
 DEFINITION ACAT related gene product 1 [Homo sapiens].
 ACCESSION AAC63997
 PID g3746533
 VERSION AAC63997.1 GI:3746533
 DBSOURCE locus AF059202 accession [AF059202.1](#)
 KEYWORDS .
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (residues 1 to 488)
 AUTHORS Oelkers, P., Behari, A., Cromley, D., Billheimer, J.T. and Sturley, S.L.
 TITLE Characterization of two human genes encoding acyl coenzyme
 A:cholesterol acyltransferase-related enzymes
 JOURNAL J. Biol. Chem. 273 (41), 26765-26771 (1998)
 MEDLINE [98434592](#)
 REFERENCE 2 (residues 1 to 488)
 AUTHORS Oelkers, P., Cromley, D., Behari, A., Billheimer, J.T. and Sturley, S.L.
 TITLE Direct Submission
 JOURNAL Submitted (13-APR-1998) Human Nutrition, Columbia University, 630
 W. 168th Street, New York, NY 10032, USA
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301 vptiqnsmkp fkdmdysrii erllklavpn hliwliffyw lfhsclnava elmqfgdref
361 yrdwnsesv tyfwqnwnip vhwcihrfy kpmlrrgssk wmartgvfla saffheylvs
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Search for

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1: AAC72917 **diacylglycerol acyltransferase [Mus musculus]**

LOCUS AAC72917 498 aa ROD 11-NOV-1998
 DEFINITION diacylglycerol acyltransferase [Mus musculus].
 ACCESSION AAC72917
 PID g3859934
 VERSION AAC72917.1 GI:3859934
 DBSOURCE locus AF078752 accession AF078752.1
 KEYWORDS .
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (residues 1 to 498)
 AUTHORS Cases, S., Smith, S.J., Zheng, Y.-W., Myers, H.M., Lear, S.R., Sande, E.,
 Novak, S., Collins, C., Welch, C.B., Lusi, A.J., Erickson, S.K. and
 Farese, R.V. Jr.
 TITLE Identification of a gene encoding an acyl CoA:diacylglycerol
 acyltransferase, a key enzyme in triacylglycerol synthesis
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (22), 13018-13023 (1998)
 MEDLINE 99007259
 REFERENCE 2 (residues 1 to 498)
 AUTHORS Farese, R.V. Jr.
 TITLE Direct Submission
 JOURNAL Submitted (16-JUL-1998) Gladstone Institute, 2550 23rd Street, San
 Francisco, CA 94110, USA
 COMMENT Method: conceptual translation supplied by author.
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 121 gilvdpigvv slflkdpysw papcviiasn ifvvaafqie krlavgalte qmglllhv
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 301 qlqvqliqqw mvptiqnsmk pfkdmrysri ierllklavp nhliwliffy wffhsclnav
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Search for

as

1: CAB44774 diacylglycerol O-acyltransferase [Arabidopsis thaliana]

LOCUS CAB44774 520 aa PLN 10-JUN-1999
 DEFINITION diacylglycerol O-acyltransferase [Arabidopsis thaliana].
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 PID g5050913
 VERSION CAB44774.1 GI:5050913
 DBSOURCE embl locus ATH131831, accession [AJ131831.1](#)
 KEYWORDS .
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 ORGANISM *Arabidopsis thaliana*
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (residues 1 to 520)
 AUTHORS Hobbs,D.H., Lu,C. and Hills,M.J.
 TITLE Cloning of a cDNA encoding diacylglycerol acyltransferase from
 Arabidopsis thaliana and its functional expression
 JOURNAL FEBS Lett. 452 (3), 145-149 (1999)
 MEDLINE [99313150](#)
 REFERENCE 2 (residues 1 to 520)
 AUTHORS Hills,M.J.
 TITLE Direct Submission
 JOURNAL Submitted (22-DEC-1998) Hills M.J., Department of Brassica and
 Oilseeds Research, John Innes Centre, Colney Lane, Norwich, NR4
 7UH, U.K

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241 lmltciwlv klvsyahtsy dirslanaad kanpevsyyv slkslayfmv aptlcyqpsy
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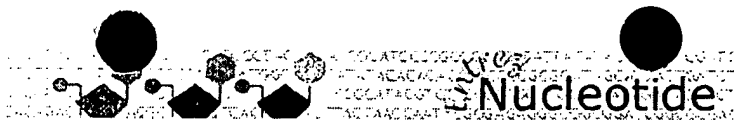
Search for

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1: AAD45536 putative diacylglycerol acyltransferase [Brassica napus]

LOCUS AF164434_1 503 aa PLN 30-NOV-1999
 DEFINITION putative diacylglycerol acyltransferase [Brassica napus].
 ACCESSION AAD45536
 PID g5579408
 VERSION AAD45536.1 GI:5579408
 DBSOURCE locus AF164434 accession AF164434.1
 KEYWORDS .
 SOURCE rape.
 ORGANISM Brassica napus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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 Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1 (residues 1 to 503)
 AUTHORS Nykiforuk, C.L., Laroche, A. and Weselake, R.J.
 TITLE Isolation and Characterization of a cDNA Encoding a Second Putative
 Diacylglycerol Acyltransferase from a Microspore-derived Cell
 Suspension Culture of Brassica napus L. cv Jet Neuf (Accession No.
 AF164434). (PGR99-158)
 JOURNAL Plant Physiol. 121 (3), 1053 (1999)
 REFERENCE 2 (residues 1 to 503)
 AUTHORS Nykiforuk, C.L., Laroche, A. and Weselake, R.J.
 TITLE Direct Submission
 JOURNAL Submitted (30-JUN-1999) Chemistry and Biochemistry, University of
 Lethbridge, 4401 University Drive, Lethbridge, Alberta T1K 3M4,
 Canada
 COMMENT Method: conceptual translation supplied by author.
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 301 lviftglmgf iieqyinpiw rnskhplkgd llyaiervlk lsvpnlyvwl cmfycffhlw
 361 lnlaellcf gdrefykdwv naksvgydwr mwnmpvhkwm vrhvyfpcir ikipkvpaii
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Search for

as

1: AC003058

LOCUS ATAC003058 97495 bp DNA PLN 16-MAY-1998
DEFINITION Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence, complete sequence.
ACCESSION AC003058
VERSION AC003058.1 GI:3135250
KEYWORDS HTG.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 97495)
AUTHORS Rounsley, S.D., Lin, X., Ketchum, K.A., Crosby, M.L., Brandon, R.C., Sykes, S.M., Kaul, S., Mason, T.M., Kerlavage, A.R., Adams, M.D., Somerville, C.R. and Venter, J.C.
TITLE Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 97495)
AUTHORS Rounsley, S.D. and Lin, X.
TITLE Direct Submission
JOURNAL Submitted (06-NOV-1997) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA, rounsley@tigr.org
REFERENCE 3 (bases 1 to 97495)
AUTHORS Rounsley, S.D.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-1998) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
COMMENT [WARNING] On Dec 17, 1999 this sequence was replaced by a newer version gi:6598388.
On May 16, 1998 this sequence version replaced gi:3128164.
Address all correspondence to:
Steve Rounsley
The Institute for Genomic Research
9712 Medical Center Dr,
Rockville, MD 20850,
USA
e-mail: rounsley@tigr.org
BAC clone F27F23 is from Arabidopsis chromosome II and is contained in the YAC clone CIC06E08.
The orientation of the sequence is from SP6 to T7 end of the BAC clone.
Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, <http://gnomic.stanford.edu/~chris/GENSCANW.html>), and NetPlantGene (<http://www.cbs.dtu.dk/netpgene/cbsnetpgene.html>), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TIGR (<http://www.tigr.org/tdb/at/at.html>). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins.

Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats are identified by repeatmasker (Arian Smit, <http://ftp.genome.washington.edu/RM/RepeatMasker.html>). Regions of genomic sequence that are not annotated as genes but have predicted exons by GRAIL are annotated as misc features.

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CDS complement(join(13430..13585,13844..15762,16010..16186,
16516..16604,16763..16944))
/gene="F27F23.4"
/note="hypothetical protein"
/codon_start=1
/protein_id="AAC16454.1"
/db_xref="GI:3135254"
/translation="MAPSEIEPALQEPGSLVLSREDRRFANLRGVRWRVNLGVLP
ASSIDEFRRRAANSRRRRRLMDPHVLKHEDSSPNFIIDNPLSQNPNSTWGQFFRNAE
LEKTLDDQLSRLYPEHWCFYQTPRYQGMRLRIILLWCLKHPEYGYRQGMHELLAPLLY
VLHVDIMRLSEVRKSYEDYFTDRFDSLSFMERDITYTFDFNKFMDSDVNDGIGSQGHSK
NFNSLDELDPVQSLVMLTDSYGTESELGIVLSEKFMHEDAYCMFDALMSGIHGCFAM
ASFFSYSPASGSHTGLTPVLEACSAFYRILAVVDSSLHSHLVELGVPEQYFGLRWLRV
LFGREFLLQDLLLVWDEIILADNSARTDEDSRNQNFRIIFDCPRGTLVLGMTVSMILYL
RSSLLSTENATCCLQRLNFPENIDLNKIIQKAKLLQALVLDTDMLSALSINGVFDQS
NFVPARTKSCSTSPRSPLIIAPESYWEKKWRVLHKAEEEEENKICLEKQTPPTQKKRW
LNVTKLFRVIDLSHHKLGIGERKANSSPVTQSLLEDSSQLNVDCHVTNKENIHPQ
ETEENIMEFHSADEESIVSGSSPSEESSFVSLDPTSPVRCSTKIENDSVSSAGSNLLP
DEDDKSIVSISEENSSVSDPISPAIDSNYSKYLDCTGSENDKDDQTSVNSPLSVS
PHRRNEYPVTQSDDEVSTDKSVGITKEYKLLHGIVQWFRKLKRTLSSEETSHRKASDA
TKTNDVKIKKNQIGCYSESHQALSSGDSSQNLRLKTLKNLGQSMCLKHIEAIELVFQQE
PCLVPAGLIGNLAKTNLIEKGQVTATTALKELRKL SNLLSEM"

mRNA join(<17068..17148,18012..18127,18236..18341,
18392..>18550)
/gene="F27F23.5"

gene <17068..>18550
/gene="F27F23.5"

CDS join(17068..17148,18012..18127,18236..18341,18392..18550)
/gene="F27F23.5"
/codon_start=1
/product="Mg-chelatase subunit D-like protein"
/protein_id="AAC16455.1"
/db_xref="GI:3135255"
/translation="MNDDENMNFVCCVRDSRREEPIDEEEQSYRCLILNIVEREGIS
FRNPCKPLLVAIYQPEEGAIQDFEDPVAAVGIAKQLQEHCEVFRMVKETNSNEHCNV
KLVSILVLKCYSMTMWISLKMTRLRMVIMILKRRKTEIALVAWEMLAMKMAT"

repeat region complement(17380..17504)
/rpt_family="(TAAA)n"

misc feature 18632..18706
/note="exon predicted by xgrail, quality good"

misc feature 19078..19123
/note="exon predicted by xgrail, quality marginal"

misc feature 19480..19517
/note="exon predicted by xgrail, quality marginal"

misc feature 19557..19652
/note="exon predicted by xgrail, quality excellent"

misc feature 19737..19810
/note="exon predicted by xgrail, quality marginal"

misc feature 19935..20056
/note="exon predicted by xgrail, quality marginal"

misc feature complement(20075..20092)
/note="exon predicted by xgrail, quality
marginal_shadowexon"

repeat region complement(20457..20499)
/rpt_family="AT_rich"

repeat region 20531..20576
/rpt_family="(GA)n"

repeat region complement(20700..20787)
/rpt_family="(CAAAA)n"

misc feature 21345..21442
/note="exon predicted by xgrail, quality good"

misc feature complement(21512..21553)
/note="exon predicted by xgrail, quality marginal_shadowexon"

misc feature 21590..21671
/note="exon predicted by xgrail, quality excellent"

mRNA join(<21713..23229,23377..23431,23522..23625,23778..23868,23909..23941,24091..24215,24233..>24269)
/gene="F27F23.6"

gene <21713..>24269
/gene="F27F23.6"

CDS /note="predicted by genscan"
join(21713..23229,23377..23431,23522..23625,23778..23868,23909..23941,24091..24215,24233..24269)
/gene="F27F23.6"
/note="hypothetical protein"
/codon_start=1
/protein_id="AAC16456.1"
/db_xref="GI:3135256"
/translation="MLVESSFSSSVETSLNLVSEYQDPFAAYDWTSLAESYQMIHKVPEQSQVSFLKNVPVTDTMNLDESKHPKHQESCSEKSVMHKVSQKALTSVYRRRKRTLI
PGGTEEHLGKIRKQDDSLDDSIIVSLYNPEESTKRKNRFNNCLVYSRKKRRGESSCTF
TGETTIRGDGLDDAFVSEHDCGETRRRGNRSDCLVYSRKKGRVKFNCSFSKHVTGR
TKISYDQADSSACSMGQIVKADSSLTRPKPGEIKKSGHQLVYSQRKQLVKSNGSFTE
SHVGKTKRNGDRSEVLLTYSRRKSGKSIGVRVNGFLVYTRKKLFRGPFARRDLSET
KKNQDQRSTVSSRELDDTQVTEVTCSSDGTNDSCSSKSSSEVNSTSSKSREDDCYS
SDSGVSETDTDGSSSPFRQCKHCDKPGTVEKMLICDECEEAYHTRCCGVQMKDVAEID
EWLCPCLKNQSSKTKTKGRISHERKWRVTVPFVIGIRIGKMFQADVPDWGPTMSDT
SFVGEPLIEIGQSEYMHDLLKAKNSKKQCSAVNWLQCREEDTNGVICGKWRRAPRSEVQ
TKDWECFCCFSWDPSRADCAVPQKNPSEDEKLAAELETSEILKQLKYIKMVRYSHYL
FDLSRPYSFLIKDLKLRLDLDTQPKSEN"

misc feature complement(24507..24590)
/note="exon predicted by xgrail, quality good_shadowexon"

mRNA complement(join(<24731..24895,25375..>26289))
/gene="F27F23.7"

gene complement(<24731..>26289)
/gene="F27F23.7"

CDS complement(join(24731..24895,25375..26289))
/gene="F27F23.7"
/note="unknown protein"
/codon_start=1
/protein_id="AAC16457.1"
/db_xref="GI:3135257"
/translation="MDSLIVASYASSDEEEDLQPRREAFTVKSSEPSASSLFSAPQPK
ELKSSDGDGLGSSSSRGKSSSFLSSLPKSSISRKKNPNPSSIPKRQVQIRLPVNPR
PSNLDDDEDEEEKARKKRKQMESASASHDSSVRSFLSAMPAPKSSQTLGALPSLGSG
SGRRSNLETETPSIAFPQTDGSDQDQNSYESFSHNSNETEQIVGVNDNYATGYDGG
YETIPSGSSVGYDGSSYGGNTWNGGGFEAMTGLPEAVVAMDSGARRGRNRNQMPEIV
EVKQDELKMNRPVVDQVKSTGIAFGPAYQPVTSSSKGVSKLHKRKHQITALFMDMKH
KESELTERRSRGLLTKAETQAKYGW"

repeat region complement(25930..25971)
/rpt_family="(GAA)n"

repeat region 26293..26327
/rpt_family="(GA)n"

mRNA <27054..>29135
/gene="F27F23.8"

gene <27054..>29135
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CDS 27054..29135
/gene="F27F23.8"

f 39

/gene="F27F23.11"
/codon_start=1
/product="putative 18.5 KDa class I heat shock protein"
/protein_id="AAC16461.1"
/db_xref="GI:3135261"
/translation="MSMIPISNRRRLSPGDRIWEPFELMNTFLDFPSPALFLSHHFPS
LSREIFPQTSSSTVNTQLNWTETPTAHVFKAYLPGVDQDEVIAFVDEEGYLQICTGDN
KFMSRFKLPNNALTDQVTAWMEDEFLVVFVEKDASSSPQLPEIEENRNVRVVEITGD
DD"
mRNA complement(<35246..>35479)
/gene="F27F23.12"
gene complement(<35246..>35479)
/gene="F27F23.12"
/note="predicted by genefinder"
CDS complement(35246..35479)
/gene="F27F23.12"
/note="hypothetical protein"
/codon_start=1
/protein_id="AAC16462.1"
/db_xref="GI:3135262"
/translation="MEATKERMEKDQKKRVVTNEAGKAEDNTIRTIIRESIVEDRGSN
DDGNGKDNHDHGASKPEDILAFSRTVVRKIDSSLE"
repeat region complement(35434..35502)
/rpt_family="(GA)n"
misc feature 35505..35714
/note="exon predicted by xgrail, quality good_shadowexon"
repeat region complement(35815..35856)
/rpt_family="AT-rich"
repeat region complement(36232..36341)
/rpt_family="(TAAAA)n"
repeat region complement(36645..36668)
/rpt_family="AT-rich"
misc feature complement(36701..36723)
/note="exon predicted by xgrail, quality
excellent_shadowexon"
repeat region 37269..37319
/rpt_family="(TA)n"
mRNA join(<37329..37616,37890..38059,38151..>38835)
/gene="F27F23.13"
gene <37329..>38835
/gene="F27F23.13"
/note="predicted by genscan"
CDS join(37329..37616,37890..38059,38151..38835)
/gene="F27F23.13"
/note="hypothetical protein"
/codon_start=1
/protein_id="AAC16463.1"
/db_xref="GI:3135263"
/translation="MICEEAYHQPPQIQKEQMMTMDQRNNHQKRSPSSPSSPSSPS
SPSSPKSPSFNNNEERLEVVNLSGMALES LPNPSLNLAQICKLDLSNNHLQTIPESL
TARLLNLIALDVHSNQIKALPNSIGCLSKLKTNLVSGNFLVSFPKSIQHCRSLEELNA
NFNKLIRLPDSIGFELTNLRKLSINSNKLISLPISITHLTSRLVLDARLNCMLIPDD
LENLINLEILNVSQNFQYLSALPSSIGLLMNLIELDVSYNKITVLPESIGCMRRLRKL
SVEGNPLVSPPIEVMEQNLQVVREYLTQKMNGGSPRSPSKKKS WGFGLVKVYGTFNNG
SRSWNREEREGFIMPEYRSIDSLASPRYSGMFSPRRLFSPTYFSR"
repeat region 37393..37488
/rpt_family="(CAT)n"
misc feature complement(39371..39466)
/note="exon predicted by xgrail, quality
marginal_shadowexon"
mRNA complement(<39656..40234)
/gene="F27F23.14"
gene complement(<39656..40234)
/gene="F27F23.14"
CDS complement(39656..40177)

/gene="F27F23.14"
/note="unknown protein"
/codon_start=1
/protein_id="AAC16464.1"
/db_xref="GI:3135264"
/translation="MAPRSDSQTGSSVSDGSDQSSMDPIFHLLRIVPFSFLRPPLRL
KIPSFITLSPMTVYALILLTYFLVVSGFVYDVIVEPPGIGSTQDPTTGTIRPVVFMMSG
RVNGQYIIIEGLSSGFVFLGGIGIVMLDLALDKNKAKSVKASYAVAGVSSIVIAVYMS
MLFIRIKIPGYLY"
misc feature 40515..40611
/note="exon predicted by xgrail, quality good"
mRNA join(40644..40900,41358..41621)
/gene="F27F23.15"
gene 40644..41621
/gene="F27F23.15"
CDS join(40711..40900,41358..41479)
/gene="F27F23.15"
/note="unknown protein"
/codon_start=1
/protein_id="AAC16465.1"
/db_xref="GI:3135265"
/translation="MAYVDHAFSISDEDLDMIGTSYTVSNRPPVKEISLAVGLLVFGTL
GIVLGFFMAYNRVGGDRGHGIFIVLGCLLFIPGFYYTRIAYYAYKGYKGFSSFNIPS
V"
misc feature complement(41924..42096)
/note="exon predicted by xgrail, quality
marginal_shadowexon"
misc feature 42333..42361
/note="exon predicted by xgrail, quality marginal"
repeat region complement(42840..42968)
/rpt_family="(TAAA)n"
repeat region 42922..42978
/rpt_family="(TA)n"
mRNA join(<43061..43198,43612..43854,45290..>45340)
/gene="F27F23.16"
gene <43061..>45340
/gene="F27F23.16"
/note="predicted by genscan"
CDS join(43061..43198,43612..43854,45290..45340)
/gene="F27F23.16"
/note="hypothetical protein"
/codon_start=1
/protein_id="AAC16466.1"
/db_xref="GI:3135266"
/translation="MANLIVLYILVIEAMIVIGSESSDSRDAEINRLKLNKPFLKS
IKMRPTSYPEGWSNKSNDNEKHKMPQLWTINGKCPKNSIPIRTRKEDILRAKSIER
FGKKDPNNIHQHKPTNPTNNDGTHEFKVETSLLIIPRKILS"
misc feature complement(45387..45443)
/note="exon predicted by xgrail, quality
marginal_shadowexon"
repeat region 45508..45622
/rpt_family="(CAAAA)n"
mRNA <46273..>46581
/gene="F27F23.17"
gene <46273..>46581
/gene="F27F23.17"
/note="predicted by genscan and genefinder"
CDS 46273..46581
/gene="F27F23.17"
/note="hypothetical protein"
/codon_start=1
/protein_id="AAC16467.1"
/db_xref="GI:3135267"
/translation="MERERGSERERERERERERERERERERERERERERERERE
REREREREREREREREREKHKPATLAKNRRRRFVKNRRRRDHRRRISIIDGYESQF

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unsure 46294..46465
/gene="F27F23.17"
/note="Unable to sequence across the GA repeat region. The size of this region was estimated from the size of 6 shotgun clones."
repeat region 46294..46413
/rpt_family="(GA)n"
repeat region 46414..46467
/rpt_family="(GA)n"
misc feature complement(46849..46920)
/note="exon predicted by xgrail, quality marginal_shadowexon"
misc feature 46851..46892
/note="exon predicted by xgrail, quality marginal"
repeat region complement(46922..46960)
/rpt_family="AT-rich"
misc feature 46982..47044
/note="exon predicted by xgrail, quality good"
misc feature 47142..47253
/note="exon predicted by xgrail, quality excellent"
misc feature complement(47175..47255)
/note="exon predicted by xgrail, quality excellent_shadowexon"
misc feature 47605..47739
/note="exon predicted by xgrail, quality excellent"
repeat region 47884..47946
/rpt_family="(TAAAA)n"
repeat region 47903..47946
/rpt_family="POLY_A"
mRNA join(<48238..48324,48412..48486,48584..48684,48805..49011,49139..49348,49825..50870,51499..51581,51712..51786,51899..52029,52237..52600,52694..52801,52901..>52963)
/gene="F27F23.18"
gene <48238..>52963
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CDS join(48238..48324,48412..48486,48584..48684,48805..49011,49139..49348,49825..50870,51499..51581,51712..51786,51899..52029,52237..52600,52694..52801,52901..52963)
/gene="F27F23.18"
/codon_start=1
/product="putative RNA-binding protein"
/protein_id="AAC16468.1"
/db_xref="GI:3135268"
/translation="MVWFQCDCCGENLKKPRLPRHMSMCTATKFSIDCGNMFGQVSV
HYHNQCITEAEKYGPMVRSNGESSKQKHDFDINAELFNSQWFCSLCNATMTCEQDYFA
HVGKKHQQEKANEVADMDYSKQSEHPAVDKNNLTQQPDLDIYVGLSNDYPWFCSLCD
INATSEQTLLAHANGKKHRVKVERFDAEQKQKQSTQHSTVDKKDYSKQQIEVDINVGL
SNCYPWFCSLCNVKATCQQNLLSHANGRKHRENVLFDATQQQOLEKTTVDDKDDTTVN
ASDGNSEQKKVDLLVSSGVANGYSQAHHKKRKLETCDETWKREVVQAEAAKGGGEQKSE
SKKAKKQDKEKKRKKDKKQTKSDSDFEHDKEDIKQLLVAYSKEELVNLIYKTAEKGSR
LISAILESADRDIQRNIFVRGFGWDTTQENLKTAFESYGEIEECVVMKDKTGRGKG
YGFVMFKTRKGAREALKRPEKMYNRIVVCNLASEKPGKAGKEQDMAEPVNIDLTAKMA
NQSEAVLPGIELGRGHVLEKMHQHQQTMDMFGQNMFPYGYSHQFPFGFDPYMGALSGN
QMLAGLPNYDLNFDNRKTKKMVWFQCEDCGESLKKPKLSCIDCGEMFGRDTPVQGHNC
ITEAEKYGPKGQSKSANGTPAKPKDISKQEPDFDINVGLSNRYPWFCSLCNTKATSQQ
TLLAHADGKKHRGKAKAFHARQQQEQSTTLDNKDGSENASNVDSEQKKVDLPASSGVA
NGESHPEKKRKLETLDDETSEGEAAKGSDDLKAKKQDHEKKINWKKLITSALKSNEDKT
LKMKKLKKLVLESIVDSGRDKSELKAELELKVNLSSRFTVDGKYVKLVAKD"
repeat region 50112..50214
/rpt_family="(GAAA)n"
misc feature 54041..54119
/note="exon predicted by xgrail, quality marginal_shadowexon"

repeat region complement(54151..54181)
/rpt_family="(GAAA)n"
misc feature 54192..54262
/note="exon predicted by xgrail, quality
marginal_shadowexon"
misc feature complement(54230..54255)
/note="exon predicted by xgrail, quality marginal"
repeat region 54297..54352
/rpt_family="(GAA)n"
mRNA complement(join(<54518..55143,55234..55456,
55563..55620,55718..55788,55988..56062,56160..56606,
57088..57176,57259..57318,57413..57486,57616..58374,
58538..58720,59316..59611,60133..60385,60462..>60859))
/gene="F27F23.19"
gene complement(<54518..>60859)
/gene="F27F23.19"
CDS complement(join(54518..55143,55234..55456,55563..55620,
55718..55788,55988..56062,56160..56606,57088..57176,
57259..57318,57413..57486,57616..58374,58538..58720,
59316..59611,60133..60385,60462..60859))
/gene="F27F23.19"
/note="unknown protein"
/codon_start=1
/protein_id="AAC16469.1"
/db_xref="GI:3135269"
/translation="MSAPGKFDYSSGGLDRPLYRSNFAAQMERSSSFRESMEHPVPSH
PIMLRTTSPIAQTDVTNFFQCLRFDPKVVAADHKSIHQGDFKRHVSIAGILGDES
GSLKGFIPSPPIPEEIKRFKAGLRENNVKARERVKIFNEASSVFNFKFFPSVPTKKRSR
PEGFSGDRSGDRLVSGPGLGKMGIGQQTLAGGFELDQQLDERPKSGVPNKRTSMM
DVRNNCIVRQSAAVDKDKEIMRVGNHNAVQGEDRTSTGIDGWETSKMKKKRSSINADC
HPNLASNKVVVDGYRDLKQGIQKPTGDSRSRVNGDSNMFRQSAGNGATGYGRSDSLSH
QTSLAGHSPLARVDSHDNSLYSEKRERSIVSDKERVNLRGVNKSNIHDEFNSSSLVSN
TKTNASVRGPRSGSGLPPKLSPLHNTSPSIEWDISGCTNKPPTLSGVTQKRMTSNR
SSSPVPTQWASQRPQKISRIARRTNLVPVSSQDEVPSYSDNISDVGCSETGFGFHKRS
PAASPQLKLKGESSFSTAALSESEESGHPEIKSKDKGKQSDVDGKAAQNI PRVSIPA
LQSRKSNKPAAGEEIGDGVRRQGRTRGRGFSSTRSLNPNPKNVKNVGTAKHLRSARPI
FDKNERKLSDRKAYKQRATATNAPTLDHFVGSNDGREELLAAVNSAINIAQNFNSF
WKQMERYFGYISDDHINFLKQQELSSMGPTPVLTSSEFDSPVFPEELATSRADSKAS
PLYQRLLSALISEDSDMGVNEDLQVDLDDDDSEFVSVLNNMEFNGFRNNERLELDESENDG
SAILFKGVDKSAHCHNGKFPDNPIDFVDIQYDKLGIDEKIYLEAQSLGISIDLMP
SNVEDEGIADIEIKKLEEAICNEGSKKKEIVDRLLKPAIEMKELQEKELDQGYEKLIE
MAYEKSASRRHHNAGGKNSNNKISKQAALAFVRRTLERCHQFEKTGKSCFSEPEIKD
MFIAGLATAEDTLMKEYNTSTSTPMGSGPSSSLALIGQNSSEYAKSSDVLPSENALL
EQTTGKEDTAWSNRVKKRELLLDVIGIGTQLSSNTKGKRSRDRDRGKGQASSRGGTNK
IGRPSLSNAKGERKTKAKPKQKTTQISPSVRVPEQPKPSLPKPNEANSEYNNLEALEE
TEPILDLSQLQIPDGLGDFDAQPGDINSWFNMDDDEEDFDMTELGIPTDDISELNIKL"
misc feature 61108..61213
/note="exon predicted by xgrail, quality
marginal_shadowexon"
misc feature complement(62172..62289)
/note="exon predicted by xgrail, quality excellent"
repeat region 62692..62765
/rpt_family="AT-rich"
repeat region complement(63242..63319)
/rpt_family="POLY_A"
repeat region 63477..63530
/rpt_family="(GAA)n"
misc feature complement(63577..63664)
/note="exon predicted by xgrail, quality marginal"
misc feature complement(63905..63963)
/note="exon predicted by xgrail, quality good"
mRNA complement(join(<64017..64084,64176..64260,
64265..64408,64479..64592,64677..64814,64993..65077,
65273..65352,65478..65721,65801..66042,66131..66214,
66302..66476,66685..>66863))

gene /gene="F27F23.20"
complement(<64017..>66863)
/gene="F27F23.20"

CDS complement(join(64017..64084,64176..64260,64265..64408,
64479..64592,64677..64814,64993..65077,65273..65352,
65478..65721,65801..66042,66131..66214,66302..66476,
66685..66863))
/gene="F27F23.20"
/codon_start=1
/product="putative protein kinase"
/protein_id="AAC16470.1"
/db_xref="GI:3135270"
/translation="MENQEEDEVVLAKVTSEVEDNFEDEGLVSNSTLEKVAAAKKYIE
NHYNRRMRHIQQRKERRWVLEQKIASLDVSEKEQLELLEDLQRKETETRLMRNRLCV
DDFDLLSIIGRGAFGEVRLCREKKTGNIYAMKKLKKSEMLSRGQVEHVRAERNLLAEV
ASDCIVKLYYSFQDPEYLYLIMEYLSGGDVMTLLMREETLTETVARFYIAQSVLAIES
IHKHNYVHRDIKPDNLLLDKYGHMKLSDFGLCKPLDCRNISAMNVNEPLNDENINESI
DGDENCISIGRRGRWKSPLQLQHWQINRRKLAYSTVGTDPDYIAPEVLLKKGYGVECD
WWSLGAIMYEMLVGYPFYSDDPVTTCKRIVSWRTHLVFPEGARLTPEARDLICRLLC
DSEHRLGSHGAGAEQIKAHTWFKDVEWEKLYEMDAAFKPVVNGELDTQNFMKFDEVEC
PKPARTGSGPSWKVLQFSGKSYIIISLIRGVLLCTYRSTGPLFLLVSITPQNINFGY
TYRNFDAVRGSRHSLDIKGSVSPRSSTDSTRKSCY"

repeat region complement(67208..67305)
/rpt_family="AT_rich"

repeat region 67324..67389
/rpt_family="AT_rich"

repeat region complement(67482..67596)
/rpt_family="(TAA)n"

repeat region 67691..67736
/rpt_family="AT_rich"

misc feature 68012..68070
/note="exon predicted by xgrail, quality
marginal_shadowexon"

misc feature complement(68027..68095)
/note="exon predicted by xgrail, quality marginal"

misc feature 68102..68180
/note="exon predicted by xgrail, quality
marginal_shadowexon"

mRNA complement(join(<69283..69483,69580..70329,
70417..70845,71074..71175,71265..71539,71929..72042,
72214..72352,72624..72796,73172..>73394))
/gene="F27F23.21"

gene complement(<69283..>73394)
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CDS complement(join(69283..69483,69580..70329,70417..70845,
71074..71175,71265..71539,71929..72042,72214..72352,
72624..72796,73172..73394))
/gene="F27F23.21"
/codon_start=1
/product="putative receptor-like protein kinase"
/protein_id="AAC16471.1"
/db_xref="GI:3135271"
/translation="MVVMLTQEMSGGGGPKAEEGQLFVAVAVKGLIGDKLGGAGSRRA
VRWAVDNLLPKADKFVMIHVIPITISIPNLIILMFTRMWVVTAGDRLPVVEEVESV
VEMYVRDVKKKEYETVFPFLKMKCKSTRSTKRYFRSRRTKGTGVPLTVLRYAPETCEVY
IVCKDRITTKSMDPLINREPTSPHAAATAHDFLRDWAASFHTLRSPTLPDRQSTEA
GTRRSASARELRFELSLTCNKPKTPQSSKASSATTPEIFRRRRGSDIPQLNYSDFDK
TCTKPQSNVENIVSEHRSDRSPPESTRSKKVEIEEEVERLKNELOSTVFYKQACE
ELFSTQNKVKMLSTEYLNESKRVNNAVEKEELQRNTAALEKERYMKAVKEVETAKALL
AREFCQRQIAEVNALRTYLEKKKVIDQLLGTDRHYRKYTIEEIVTATEGFSPEKVICE
GGYGKVVYQCSLDSTPAAVKVVRLDTPEKKQEFLKEVEVLSQLRHPHVLLLLGACPENG
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CDS complement(join(82546..83159,83227..83726,83782..84188))
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excellent_shadowexon"
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